

D.Krose
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TECH CENTER 1600/2900



1638

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/697,719

DATE: 05/21/2002

TIME: 13:32:37

Input Set : A:\0020-4764P.st25A.txt

Output Set: N:\CRF3\05212002\I697719.raw

P.6

3 <110> APPLICANT: NAKAJIMA, Hiroki
4 NAGASAWA, Akitsu
6 <120> TITLE OF INVENTION: Method for giving resistance to weed control compounds to
plants
8 <130> FILE REFERENCE: 0020-4764P
10 <140> CURRENT APPLICATION NUMBER: 09/697,719
11 <141> CURRENT FILING DATE: 2000-10-27
13 <150> PRIOR APPLICATION NUMBER: JP 10/120553
14 <151> PRIOR FILING DATE: 1998-04-30
16 <150> PRIOR APPLICATION NUMBER: JP 10/281127
17 <151> PRIOR FILING DATE: 1998-10-02
19 <150> PRIOR APPLICATION NUMBER: JP 10/330981
20 <151> PRIOR FILING DATE: 1998-11-20
22 <150> PRIOR APPLICATION NUMBER: JP 11/054730
23 <151> PRIOR FILING DATE: 1999-03-02
25 <160> NUMBER OF SEQ ID NOS: 78
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 39
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify bchH gene
35 <400> SEQUENCE: 1
36 gacatctaga ggagacgacc atatgcacgg tgaagtctc 39
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 31
40 <212> TYPE: DNA
41 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify bchH gene
46 <400> SEQUENCE: 2
47 acggaaacctt agatcttcac tcggcgccaa t 31
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 39
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify soybean PPO gene
57 <400> SEQUENCE: 3
58 tcgagctcca tggttccgt cttcaacgag atcctattc 39
60 <210> SEQ ID NO: 4
61 <211> LENGTH: 36
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence

ENTERED

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65 <220> FEATURE:
 66 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify soybean PPO gene
 68 <400> SEQUENCE: 4
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 71 <210> SEQ ID NO: 5
 72 <211> LENGTH: 1632
 73 <212> TYPE: DNA
 74 <213> ORGANISM: Glycine max var. Williams82
 76 <220> FEATURE:
 77 <221> NAME/KEY: CDS
 78 <222> LOCATION: (1)...(1632)
 80 <400> SEQUENCE: 5
 81 atg gtt tcc gtc ttc aac gag atc cta ttc ccg ccg aac caa acc ctt 48
 82 Met Val Ser Val Phe Asn Glu Ile Leu Phe Pro Pro Asn Gln Thr Leu
 83 1 5 10 15
 84 ctt cgc ccc tcc ctc cat tcc cca acc tct ttc ttc acc tct ccc act 96
 85 Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr
 86 20 25 30
 87 cga aaa ttc cct cgc tct cgc cct aac cct att cta cgc tgc tcc att 144
 88 Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile
 89 35 40 45
 90 gcg gag gaa tcc acc gcg tct ccg ccc aaa acc aga gac tcc gcc ccc 192
 91 Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro
 92 50 55 60
 93 gtg gac tgc gtc gtc ggc gga ggc gtc agc ggc ctc tgc atc gcc 240
 94 Val Asp Cys Val Val Gly Gly Val Ser Gly Leu Cys Ile Ala
 95 65 70 75 80
 96 cag gcc ctc gcc acc aaa cac gcc aat gcc aac gtc gtc gtc acg gag 288
 97 Gln Ala Leu Ala Thr Lys His Ala Asn Ala Val Val Val Thr Glu
 98 85 90 95
 99 gcc cga gac cgc gtc ggc aac atc acc acg atg gag agg gac gga 336
 100 Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly
 101 100 105 110
 102 tac ctc tgg gaa gaa ggc ccc aac agc ttc cag cct tct gat cca atg 384
 103 Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met
 104 115 120 125
 105 ctc acc atg gtg gtc gac agt ggt tta aag gat gag ctt gtt ttg ggg 432
 106 Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly
 107 130 135 140
 108 gat cct gat gca cct cgg ttt gtg ttg tgg aac agg aag ttg agg ccg 480
 109 Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro
 110 145 150 155 160
 111 gtg ccc ggg aag ctg act gat ttg cct ttc gac ttg atg agc att 528
 112 Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile
 113 165 170 175
 114 ggt ggc aaa atc agg gct ggc ttt ggt gcg ctt gga att cgg cct cct 576
 115 Gly Gly Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Pro
 116 180 185 190
 117 cct cca ggt cat gag gaa tcg gtt gaa gag ttt gtt cgt cgg aac ctt 624

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Input Set : A:\0020-4764P.st25A.txt
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118	Pro	Pro	Gly	His	Glu	Glu	Ser	Val	Glu	Glu	Phe	Val	Arg	Arg	Asn	Leu	
119					195				200				205				
120	ggt	gat	gag	gtt	ttt	gaa	cgg	ttg	ata	gag	cct	ttt	tgt	tca	ggg	gtc	
121	Gly	Asp	Glu	Val	Phe	Glu	Arg	Leu	Ile	Glu	Pro	Phe	Cys	Ser	Gly	Val	
122					210				215			220					
123	tat	gca	ggc	gat	cct	tca	aaa	tta	agt	atg	aaa	gca	tcc	ggg	aaa		
124	Tyr	Ala	Gly	Asp	Pro	Ser	Lys	Leu	Ser	Met	Lys	Ala	Ala	Phe	Gly	Lys	
125	225					230				235			240				
126	gtt	tgg	aag	ctg	gaa	aaa	aat	ggt	ggc	att	att	ggt	gga	act	ttc		
127	Val	Trp	Lys	Leu	Glu	Lys	Asn	Gly	Gly	Ser	Ile	Ile	Gly	Gly	Thr	Phe	
128						245				250			255				
129	aaa	gca	ata	caa	gag	aga	aat	gga	gct	tca	aaa	cca	cct	cga	gat	ccg	
130	Lys	Ala	Ile	Gln	Glu	Arg	Asn	Gly	Ala	Ser	Lys	Pro	Pro	Arg	Asp	Pro	
131						260				265			270				
132	cgt	ctg	cca	aaa	cca	aaa	ggt	cag	act	gtt	gga	tct	ttc	cgx	aag	gga	
133	Arg	Leu	Pro	Lys	Pro	Lys	Gly	Gln	Thr	Val	Gly	Ser	Phe	Arg	Lys	Gly	
134						275				280			285				
135	ctt	acc	atg	ttg	cct	gat	gca	att	tct	gcc	aga	cta	ggc	aac	aaa	gta	
136	Leu	Thr	Met	Leu	Pro	Asp	Ala	Ile	Ser	Ala	Arg	Leu	Gly	Asn	Lys	Val	
137						290				295			300				
138	aag	tta	tct	tgg	aag	ctt	tca	agt	att	agt	aaa	ctg	gat	agt	gga	gag	
139	Lys	Leu	Ser	Trp	Lys	Leu	Ser	Ser	Ile	Ser	Lys	Leu	Asp	Ser	Gly	Glu	
140	305					310				315			320				
141	tac	agt	ttg	aca	tat	gaa	aca	cca	gaa	gga	gtg	gtt	tct	ttg	cag	tgc	
142	Tyr	Ser	Leu	Thr	Tyr	Glu	Thr	Pro	Glu	Gly	Val	Val	Ser	Leu	Gln	Cys	
143						325				330			335				
144	aaa	act	gtt	gtc	ctg	acc	att	cct	tcc	tat	gtt	gct	agt	aca	ttg	ctg	
145	Lys	Thr	Val	Val	Leu	Thr	Ile	Pro	Ser	Tyr	Val	Ala	Ser	Thr	Leu	Leu	
146						340				345			350				
147	cgt	cct	ctg	tct	gtc	gtc	gtc	gca	gat	gca	ctt	tca	aag	ttt	ttt	tat	
148	Arg	Pro	Leu	Ser	Ala	Ala	Ala	Asp	Ala	Leu	Ser	Lys	Phe	Tyr	Tyr		
149						355				360			365				
150	cct	cca	gtt	gct	gca	gtt	tcc	ata	tcc	tat	cca	aaa	gaa	gct	att	aga	
151	Pro	Pro	Val	Ala	Ala	Val	Ser	Ile	Ser	Tyr	Pro	Lys	Glu	Ala	Ile	Arg	
152						370				375			380				
153	tca	gaa	tgc	ttg	ata	gat	ggt	gag	ttg	aag	ggg	ttt	ggt	caa	ttg	cat	
154	Ser	Glu	Cys	Leu	Ile	Asp	Gly	Glu	Leu	Lys	Gly	Phe	Gly	Gln	Leu	His	
155						385				390			395		400		
156	cca	cgt	agc	caa	gga	gtg	gaa	aca	tta	gga	act	ata	tac	agc	tca	tca	
157	Pro	Arg	Ser	Gln	Gly	Val	Glu	Thr	Leu	Gly	Thr	Ile	Tyr	Ser	Ser	Ser	
158						405				410			415				
159	cta	ttc	ccc	aac	cga	gca	cca	cct	gga	agg	gtt	cta	ctc	ttg	aat	tac	
160	Leu	Phe	Pro	Asn	Arg	Ala	Pro	Pro	Gly	Arg	Val	Leu	Leu	Asn	Tyr		
161						420				425			430				
162	att	gga	gga	gca	act	aat	act	gga	att	tta	tcg	aag	acg	gac	agt	gaa	
163	Ile	Gly	Gly	Ala	Thr	Asn	Thr	Gly	Ile	Leu	Ser	Lys	Thr	Asp	Ser	Glu	
164						435				440			445				
165	ctt	gtg	gaa	aca	gta	gtt	gat	cga	gat	ttg	agg	aaa	atc	ctt	ata	aac	cca
166	Leu	Val	Glu	Thr	Val	Asp	Arg	Asp	Leu	Arg	Lys	Ile	Leu	Ile	Asn	Pro	

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167	450	455	460	
168	aat gcc cag gat cca ttt gta gtg ggg gtg aga ctg tgg cct caa gct			1440
169	Asn Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala			
170	465	470	475	480
171	att cca cag ttc tta gtt ggc cat ctt gat ctt cta gat gtt gct aaa			1488
172	Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys			
173	485	490	495	
174	gct tct atc aga aat act ggg ttt gaa ggg ctc ttc ctt ggg ggt aat			1536
175	Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Asn			
176	500	505	510	
177	tat gtg tct ggt gtt gcc ttg gga cga tgc gtt gag gga gcc tat gag			1584
178	Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu			
179	515	520	525	
180	gta gca gct gaa gta aac gat ttt ctc aca aat aga gtg tac aaa tag			1632
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182	530	535	540	543
184	<210> SEQ ID NO: 6			
185	<211> LENGTH: 543			
186	<212> TYPE: PRT			
187	<213> ORGANISM: Glycine max var. Williams82			
189	<400> SEQUENCE: 6			
190	Met Val Ser Val Phe Asn Glu Ile Leu Phe Pro Pro Asn Gln Thr Leu			
191	1	5	10	15
192	Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr			
193	20	25	30	
194	Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile			
195	35	40	45	
196	Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro			
197	50	55	60	
198	Val Asp Cys Val Val Val Gly Gly Val Ser Gly Leu Cys Ile Ala			
199	65	70	75	80
200	Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu			
201	85	90	95	
202	Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly			
203	100	105	110	
204	Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met			
205	115	120	125	
206	Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly			
207	130	135	140	
208	Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro			
209	145	150	155	160
210	Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile			
211	165	170	175	
212	Gly Gly Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Pro			
213	180	185	190	
214	Pro Pro Gly His Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn Leu			
215	195	200	205	
216	Gly Asp Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val			
217	210	215	220	

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218 Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys
219 225 230 235 240
220 Val Trp Lys Leu Glu Lys Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe
221 245 250 255
222 Lys Ala Ile Gln Glu Arg Asn Gly Ala Ser Lys Pro Pro Arg Asp Pro
223 260 265 270
224 Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly
225 275 280 285
226 Leu Thr Met Leu Pro Asp Ala Ile Ser Ala Arg Leu Gly Asn Lys Val
227 290 295 300
228 Lys Leu Ser Trp Lys Leu Ser Ser Ile Ser Lys Leu Asp Ser Gly Glu
229 305 310 315 320
230 Tyr Ser Leu Thr Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Cys
231 325 330 335
232 Lys Thr Val Val Leu Thr Ile Pro Ser Tyr Val Ala Ser Thr Leu Leu
233 340 345 350
234 Arg Pro Leu Ser Ala Ala Ala Asp Ala Leu Ser Lys Phe Tyr Tyr
235 355 360 365
236 Pro Pro Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg
237 370 375 380
238 Ser Glu Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His
239 385 390 395 400
240 Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser
241 405 410 415
242 Leu Phe Pro Asn Arg Ala Pro Pro Gly Arg Val Leu Leu Leu Asn Tyr
243 420 425 430
244 Ile Gly Gly Ala Thr Asn Thr Gly Ile Leu Ser Lys Thr Asp Ser Glu
245 435 440 445
246 Leu Val Glu Thr Val Asp Arg Asp Leu Arg Lys Ile Leu Ile Asn Pro
247 450 455 460
248 Asn Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala
249 465 470 475 480
250 Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys
251 485 490 495
252 Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn
253 500 505 510
254 Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu
255 515 520 525
256 Val Ala Ala Glu Val Asn Asp Phe Leu Thr Asn Arg Val Tyr Lys
257 530 535 540 543
259 <210> SEQ ID NO: 7
260 <211> LENGTH: 39
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify bchH gene
267 <400> SEQUENCE: 7
268 gacatctagt ctagacgacc atatgcacgg tgaagtctc 39
270 <210> SEQ ID NO: 8

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/697,719

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Input Set : A:\0020-4764P.st25A.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:27; N Pos. 6,7,9,10,12,13,15,16,18,19
Seq#:28; N Pos. 8,9,11,12,14,15,17,18,20,21
Seq#:77; Xaa Pos. 2,4,5

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:9; Line(s) 287
Seq#:10; Line(s) 298
Seq#:11; Line(s) 309
Seq#:12; Line(s) 320
Seq#:13; Line(s) 331
Seq#:14; Line(s) 342
Seq#:19; Line(s) 576
Seq#:20; Line(s) 587
Seq#:21; Line(s) 598
Seq#:22; Line(s) 609
Seq#:27; Line(s) 664
Seq#:28; Line(s) 680
Seq#:29; Line(s) 696
Seq#:30; Line(s) 707
Seq#:31; Line(s) 718
Seq#:32; Line(s) 729
Seq#:33; Line(s) 740
Seq#:34; Line(s) 751
Seq#:35; Line(s) 762
Seq#:36; Line(s) 773
Seq#:37; Line(s) 784
Seq#:38; Line(s) 795
Seq#:39; Line(s) 806
Seq#:40; Line(s) 817
Seq#:41; Line(s) 828
Seq#:42; Line(s) 839
Seq#:43; Line(s) 850
Seq#:44; Line(s) 861
Seq#:45; Line(s) 872
Seq#:46; Line(s) 883
Seq#:47; Line(s) 894
Seq#:48; Line(s) 905
Seq#:49; Line(s) 916
Seq#:50; Line(s) 927
Seq#:51; Line(s) 938
Seq#:52; Line(s) 949